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1600

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/521,195B

DATE: 07/03/2002 P-6
 TIME: 14:04:33

Input Set : A:\06501-057001.txt
 Output Set: N:\CRF3\07032002\I521195B.raw

3 <110> APPLICANT: Nezu, Jun-Ichi
 4 Oku, Asuka
 6 <120> TITLE OF INVENTION: TRANSPORTER GENES
 8 <130> FILE REFERENCE: 06501-057001
 10 <140> CURRENT APPLICATION NUMBER: 09/521,195B
 11 <141> CURRENT FILING DATE: 2000-03-07
 13 <150> PRIOR APPLICATION NUMBER: JP 10/156660
 14 <151> PRIOR FILING DATE: 1998-05-20
 16 <150> PRIOR APPLICATION NUMBER: JP 9/260972
 17 <151> PRIOR FILING DATE: 1997-09-08
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04009
 20 <151> PRIOR FILING DATE: 1998-09-07
 22 <160> NUMBER OF SEQ ID NOS: 33
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 551
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro
 31 1 5 10 15
 32 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 33 20 25 30
 34 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35 35 40 45
 36 Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
 37 50 55 60
 38 Asn Ser Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser
 39 65 70 75 80
 40 Cys Ser Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
 41 85 90 95
 42 Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
 43 100 105 110
 44 Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Val
 45 115 120 125
 46 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asn Trp Lys Val Pro Leu
 47 130 135 140
 48 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Val Ser
 49 145 150 155 160
 50 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Ala Thr
 51 165 170 175
 52 Met Ala Val Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Ile Ser
 53 180 185 190
 54 Trp Glu Met Phe Thr Val Leu Phe Val Ile Val Gly Met Gly Gln Ile

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55	195	200	205
56	Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Gly Lys		
57	210	215	220
58	Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala		
59	225	230	235
60	240		
61	Val Gly Tyr Met Leu Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp		
62	245	250	255
63	Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Val Pro		
64	260	265	270
65	Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg		
66	275	280	285
67	Arg Phe Arg Glu Ala Glu Asp Ile Ile Gln Lys Ala Ala Lys Met Asn		
68	290	295	300
69	Asn Thr Ala Val Pro Ala Val Ile Phe Asp Ser Val Glu Glu Leu Asn		
70	305	310	315
71	Pro Leu Lys Gln Gln Lys Ala Phe Ile Leu Asp Leu Phe Arg Thr Arg		
72	325	330	335
73	Asn Ile Ala Ile Met Thr Ile Met Ser Leu Leu Leu Trp Met Leu Thr		
74	340	345	350
75	Ser Val Gly Tyr Phe Ala Leu Ser Leu Asp Ala Pro Asn Leu His Gly		
76	355	360	365
77	Asp Ala Tyr Leu Asn Cys Phe Leu Ser Ala Leu Ile Glu Ile Pro Ala		
78	370	375	380
79	Tyr Ile Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg Tyr Ile		
80	385	390	395
81	400		400
82	Ile Ala Ala Val Leu Phe Trp Gly Gly Val Leu Leu Phe Ile Gln		
83	405	410	415
84	Leu Val Pro Val Asp Tyr Tyr Phe Leu Ser Ile Gly Leu Val Met Leu		
85	420	425	430
86	Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val Phe Thr		
87	435	440	445
88	Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly Val Thr		
89	450	455	460
90	Ser Thr Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe Val Tyr		
91	465	470	475
92	480		
93	Leu Gly Ala Tyr Asn Arg Met Leu Pro Tyr Ile Val Met Gly Ser Leu		
94	485	490	495
95	Thr Val Leu Ile Gly Ile Phe Thr Leu Phe Phe Pro Glu Ser Leu Gly		
96	500	505	510
97	Met Thr Leu Pro Glu Thr Leu Glu Gln Met Gln Lys Val Lys Trp Phe		
98	515	520	525
99	Arg Ser Gly Lys Lys Thr Arg Asp Ser Met Glu Thr Glu Glu Asn Pro		
100	530	535	540
101	Lys Val Leu Ile Thr Ala Phe		
102	<210> SEQ ID NO: 2		
103	<211> LENGTH: 2135		
104	<212> TYPE: DNA		
	<213> ORGANISM: Homo sapiens		

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106 <220> FEATURE:

107 <221> NAME/KEY: CDS

108 <222> LOCATION: (147)..(1799)

110 <400> SEQUENCE: 2

111 ccccggttc	gccccta	ttctaacagc	ctgcctgtcc	cccgaaacg	ttctaacatc	60
112 ctggggagc	gccccagta	caagacactg	tcctgagaac	gctgtcatca	cccgtagttg	120
113 caagttcgg	agcggcagtg	ggaagc	atg	cgg	gac tac gag gtg atc gcc	173
114					Met Arg Asp Tyr Asp Glu Val Ile Ala	
115	1			5		
116 ttc ctg ggc gag	tgg	ccc ttc	cag	cgc	ctc atc ttc ttc ctg ctc	221
117 Phe Leu Gly	Glu Trp	Gly Pro	Phe Gln	Arg Leu	Ile Phe Phe Leu Leu	
118 10	15			20		25
119 agc gcc agc atc atc	ccc aat	ggc ttc aat	ggt	atg	tca gtc gtg ttc	269
120 Ser Ala Ser Ile Ile	Pro Asn Gly	Phe Asn Gly	Met Ser Val	Val Phe		
121	30		35		40	
122 ctg gcg ggg acc ccg gag	cac	cgc tgt	cga	gtg	ccg gac gcc gcg aac	317
123 Leu Ala Gly Thr Pro	Glu His Arg	Cys Arg	Val Pro	Asp Ala Ala Asn		
124	45		50		55	
125 ctg agc agc gcc tgg	cgc aac	aat agt	gtc ccg	ctg cgg	ctg cgg gac	365
126 Leu Ser Ser Ala Trp	Arg Asn Asn	Ser Val Pro	Leu Arg	Leu Arg Asp		
127	60		65		70	
128 ggc cgc gag	gtg ccc	cac agc tgc	agc cgc	tac	ccg ctc gcc acc atc	413
129 Gly Arg Glu Val	Pro His Ser	Cys Ser Arg	Tyr Arg	Leu Ala Thr Ile		
130	75		80		85	
131 gcc aac ttc tcg	gcg ctc	ggg ctg gag	ccg ggg	cgc gac	gtg gac ctg	461
132 Ala Asn Phe	Ser Ala Leu	Gly Leu Glu	Pro Gly	Arg Asp Val	Asp Leu	
133	90		95		100	105
134 ggg cag	ctg gag	cag gag	agc tgc	ctg gat	ggc tgg gag ttc	509
135 Gly Gln Leu	Glu Gln Glu	Ser Cys Leu	Asp Gly	Trp Glu	Phe Ser Gln	
136	110		115		120	
137 gac gtc tac	ctg tcc acc	gtc gtg acc	gag tgg	aat ctg	gtg tgt gag	557
138 Asp Val Tyr	Leu Ser Thr	Val Val Thr	Glu Trp	Asn Leu	Val Cys Glu	
139	125		130		135	
140 gac aac tgg aag	gtg ccc ctc	acc acc tcc	ctg ttc	gtt ggc	gtg	605
141 Asp Asn Trp	Lys Val Pro	Leu Thr Thr	Ser Leu	Phe Phe	Val Gly Val	
142	140		145		150	
143 ctc ctc ggc tcc	tcc gtg	tcc ggg	cag ctg	tca gac	agg ttt ggc agg	653
144 Leu Leu Gly	Ser Phe Val	Ser Gly Gln	Leu Ser	Asp Arg Phe	Gly Arg	
145	155		160		165	
146 aag aac gtt	ctc ttc	gca acc	atg gct	gta cag	act ggc ttc	701
147 Lys Asn Val	Leu Phe Ala	Thr Met Ala	Val Gln	Thr Gly	Phe Ser Phe	
148	170		175		180	185
149 ctg cag att	tcc atc	agc tgg	gag atg	ttc act	gtg tta ttt gtc	749
150 Leu Gln Ile	Phe Ser Ile	Ser Trp	Glu Met	Phe Thr	Val Leu Phe Val	
151	190		195		200	
152 atc gtg ggc	atg ggc	cag atc	tcc aac	tat gtg	gta gcc ttc	797
153 Ile Val Gly	Met Gly Gln	Ile Ser	Asn Tyr	Val Val	Ala Phe Ile Leu	
154	205		210		215	
155 gga aca gaa	att ctt	ggc aag	tca gtt	cgt att	ata ttc tct	845
					aca tta	

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156	Gly	Thr	Glu	Ile	Leu	Gly	Lys	Ser	Val	Arg	Ile	Ile	Phe	Ser	Thr	Leu	
157	220				225												893
158	gga	gtg	tgc	aca	ttt	ttt	gca	gtt	ggc	tat	atg	ctg	ctg	cca	ctg	ttt	
159	Gly	Val	Cys	Thr	Phe	Phe	Ala	Val	Gly	Tyr	Met	Leu	Leu	Pro	Leu	Phe	
160	235				240											245	
161	gct	tac	ttc	atc	aga	gac	tgg	cgg	atg	ctg	ctg	ctg	gcg	ctg	acg	gtg	
162	Ala	Tyr	Phe	Ile	Arg	Asp	Trp	Arg	Met	Leu	Leu	Leu	Ala	Leu	Thr	Val	
163	250				255											265	
164	ccg	gga	gtg	ctg	tgt	gtc	ccg	ctg	tgg	tgg	ttc	att	cct	gaa	tct	ccc	
165	Pro	Gly	Val	Leu	Cys	Val	Pro	Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	
166	270				275											280	
167	cga	tgg	ctg	ata	tcc	cag	aga	aga	ttt	aga	gag	gct	gaa	gat	atc	atc	
168	Arg	Trp	Leu	Ile	Ser	Gln	Arg	Arg	Phe	Arg	Glu	Ala	Glu	Asp	Ile	Ile	
169	285				290											295	
170	caa	aaa	gct	gca	aaa	atg	aac	aac	aca	gct	gta	cca	gca	gtg	ata	ttt	
171	Gln	Lys	Ala	Ala	Lys	Met	Asn	Asn	Thr	Ala	Val	Pro	Ala	Val	Ile	Phe	
172	300				305											310	
173	gat	tct	gtg	gag	gag	cta	aat	ccc	ctg	aag	cag	cag	aaa	gct	ttc	att	
174	Asp	Ser	Val	Glu	Glu	Leu	Asn	Pro	Leu	Lys	Gln	Gln	Lys	Ala	Phe	Ile	
175	315				320											325	
176	ctg	gac	ctg	ttc	agg	act	cg	aat	att	gcc	ata	atg	acc	att	atg	tct	
177	Leu	Asp	Leu	Phe	Arg	Thr	Arg	Asn	Ile	Ala	Ile	Met	Thr	Ile	Met	Ser	
178	330				335											340	345
179	ttg	ctg	cta	tgg	atg	ctg	acc	tca	gtg	ggt	tac	ttt	gct	ctg	tct	ctg	
180	Leu	Leu	Leu	Trp	Met	Leu	Thr	Ser	Val	Gly	Tyr	Phe	Ala	Leu	Ser	Leu	
181	350				355											360	
182	gat	gct	cct	aat	tta	cat	gga	gat	gcc	tac	ctg	aac	tgt	ttc	ctc	tct	
183	Asp	Ala	Pro	Asn	Leu	His	Gly	Asp	Ala	Tyr	Leu	Asn	Cys	Phe	Leu	Ser	
184	365				370											375	
185	gcc	ttg	att	gaa	att	cca	gct	tac	att	aca	gcc	tgg	ctg	cta	ttg	cga	
186	Ala	Leu	Ile	Glu	Ile	Pro	Ala	Tyr	Ile	Thr	Ala	Trp	Leu	Leu	Leu	Arg	
187	380				385											390	
188	acg	ctg	ccc	agg	cgt	tat	atc	ata	gct	gca	gta	ctg	ttc	tgg	gga	gga	
189	Thr	Leu	Pro	Arg	Arg	Tyr	Ile	Ile	Ala	Ala	Val	Leu	Phe	Trp	Gly	Gly	
190	395				400											405	
191	ggt	gtg	ctt	ctc	ttc	att	caa	ctg	gta	cct	gtg	gat	tat	tac	ttc	tta	
192	Gly	Val	Leu	Leu	Phe	Ile	Gln	Leu	Val	Pro	Val	Asp	Tyr	Tyr	Phe	Leu	
193	410				415											420	425
194	tcc	att	ggt	ctg	gtc	atg	ctg	gga	aaa	ttt	ggg	atc	acc	tct	gct	ttc	
195	Ser	Ile	Gly	Leu	Val	Met	Leu	Gly	Lys	Phe	Gly	Ile	Thr	Ser	Ala	Phe	
196	430				435											440	
197	tcc	atg	ctg	tat	gtc	ttc	act	gct	gag	ctc	tac	cca	acc	ctg	gtc	agg	
198	Ser	Met	Leu	Tyr	Val	Phe	Thr	Ala	Glu	Leu	Tyr	Pro	Thr	Leu	Val	Arg	
199	445				450											455	
200	aac	atg	gct	gtg	ggg	gtc	aca	tcc	acg	gcc	tcc	aga	gtg	ggc	agc	atc	
201	Asn	Met	Ala	Val	Gly	Val	Thr	Ser	Thr	Ala	Ser	Arg	Val	Gly	Ser	Ile	
202	460				465											470	
203	att	gcc	ccc	tac	ttt	gtt	tac	ctc	ggt	gct	tac	aac	aga	atg	ctg	ccc	
204	Ile	Ala	Pro	Tyr	Phe	Val	Tyr	Leu	Gly	Ala	Tyr	Asn	Arg	Met	Leu	Pro	

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205	475	480	485	
206	tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt			1661
207	Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu			
208	490	495	500	505
209	ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag			1709
210	Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln			
211	510	515	520	
212	atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca			1757
213	Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser			
214	525	530	535	
215	atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc			1799
216	Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe			
217	540	545	550	
219	tgaaaaata tctacccat ttggtaagt gaaaaacaga aaaataagac cctgtggaga			1859
220	aattcggtgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaacctgc			1919
221	tatcaagaaa tgctcgtcat acagtaact ctggatgatt cttccagata atgtccctgc			1979
222	tttacaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg			2039
223	taagatgtct tgaaaacatg tttagtcaagg actgtaaaa tacatataaaa gattaacact			2099
224	catttccaat catacaaata ctatccaaat aaaaat			2135
226	<210> SEQ ID NO: 3			
227	<211> LENGTH: 557			
228	<212> TYPE: PRT			
229	<213> ORGANISM: Homo sapiens			
231	<400> SEQUENCE: 3			
232	Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro			
233	1	5	10	15
234	Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn			
235	20	25	30	
236	Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu His			
237	35	40	45	
238	Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn			
239	50	55	60	
240	His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser			
241	65	70	75	80
242	Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly			
243	85	90	95	
244	Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser			
245	100	105	110	
246	Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Ile			
247	115	120	125	
248	Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro Leu			
249	130	135	140	
250	Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile Ser			
251	145	150	155	160
252	Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val Thr			
253	165	170	175	
254	Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys Asn			
255	180	185	190	
256	Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln Ile			

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 1,2,3,4,5,6,7,10,11,12,13,14

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 428
Seq#:6; Line(s) 439
Seq#:7; Line(s) 450
Seq#:8; Line(s) 461
Seq#:9; Line(s) 472
Seq#:10; Line(s) 483
Seq#:11; Line(s) 494
Seq#:12; Line(s) 505
Seq#:13; Line(s) 516
Seq#:14; Line(s) 527
Seq#:15; Line(s) 538
Seq#:16; Line(s) 549
Seq#:17; Line(s) 560
Seq#:18; Line(s) 571
Seq#:19; Line(s) 582
Seq#:20; Line(s) 593
Seq#:21; Line(s) 604
Seq#:24; Line(s) 815
Seq#:25; Line(s) 826
Seq#:26; Line(s) 837
Seq#:30; Line(s) 1057
Seq#:31; Line(s) 1068
Seq#:32; Line(s) 1079

VERIFICATION SUMMARY

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L:1092 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1096 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1100 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1104 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1112 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1116 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1120 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1124 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0